



## SEQUENCE LISTING

&lt;11&gt; RASTELLI, LUCA

<120> NOVEL SPHINGOSINE KINASES AND NUCLEIC ACIDS ENCODING  
SAME

&lt;130&gt; 10716-08

&lt;140&gt; 09/784,810

&lt;141&gt; 2001-02-14

&lt;150&gt; 60/182,360

&lt;151&gt; 2000-02-14

&lt;150&gt; 60/191,261

&lt;151&gt; 2000-03-22

&lt;160&gt; 29

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 1600

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; modified\_base

&lt;222&gt; (1)

&lt;223&gt; a, t, c, g, other or unknown

&lt;400&gt; 1

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<210> 2  
 <211> 384  
 <212> PRT  
 <213> Homo sapiens

<400> 2  
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 Val Leu Val Leu Leu Asn Pro Arg Gly Gly Lys Gly Lys Ala Leu Gln  
                   20                  25                  30  
 Leu Phe Arg Ser His Val Gln Pro Leu Leu Ala Glu Ala Glu Ile Ser  
           35                  40                  45  
 Phe Thr Leu Met Leu Thr Glu Arg Arg Asn His Ala Arg Glu Leu Val  
       50                  55                  60  
 Arg Ser Glu Glu Leu Gly Arg Trp Asp Ala Leu Val Val Met Ser Gly  
   65                  70                  75                  80  
 Asp Gly Leu Met His Glu Val Val Asn Gly Leu Met Glu Arg Pro Asp  
                   85                  90                  95  
 Trp Glu Thr Ala Ile Gln Lys Pro Leu Cys Ser Leu Pro Ala Gly Ser  
           100                  105                  110  
 Gly Asn Ala Leu Ala Ala Ser Leu Asn His Tyr Ala Gly Tyr Glu Gln  
           115                  120                  125  
 Val Thr Asn Glu Asp Leu Leu Thr Asn Cys Thr Leu Leu Leu Cys Arg  
   130                  135                  140  
 Pro Val Leu Ser Pro Met Asn Leu Leu Ser Leu His Thr Ala Ser Gly  
  145                  150                  155                  160  
 Leu Arg Ser Phe Ser Val Leu Ser Leu Ala Trp Gly Phe Ile Ala Asp  
           165                  170                  175  
 Val Asp Leu Glu Ser Asp Lys Tyr Arg Arg Leu Gly Glu Met Arg Phe  
   180                  185                  190  
 Thr Leu Gly Thr Phe Leu Arg Leu Ala Ala Leu Arg Thr Tyr Arg Gly  
   195                  200                  205  
 Arg Leu Ala Thr Leu Pro Val Gly Arg Val Gly Phe Lys Thr Pro Ala  
   210                  215                  220  
 Ser Pro Val Val Val Gln Gln Gly Pro Val Asp Ala His Leu Val Pro  
  225                  230                  235                  240  
 Leu Glu Glu Gln Val Pro Ser His Trp Gln Val Val Pro Asp Glu Asp  
           245                  250                  255

Phe Val Leu Val Leu Ala Leu Leu His Ser His Leu Ala Ser Glu Met  
 260 265 270

Phe Ala Ala Pro Met Gly Arg Cys Ala Ala Gly Val Met His Leu Phe  
 275 280 285

Tyr Val Arg Ala Gly Val Ser Arg Ala Met Leu Leu Arg Leu Phe Leu  
 290 295 300

Ala Met Glu Lys Gly Arg His Met Glu Tyr Glu Cys Pro Tyr Leu Val  
 305 310 315 320

Tyr Val Pro Val Val Ala Phe Arg Leu Glu Pro Lys Asp Gly Lys Gly  
 325 330 335

Val Phe Ala Val Asp Gly Glu Leu Met Val Ser Glu Ala Val Gln Gly  
 340 345 350

Gln Val His Pro Asn Tyr Phe Trp Met Val Ser Gly Cys Val Glu Pro  
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Pro Pro Ser Trp Lys Pro Gln Gln Met Pro Pro Pro Glu Glu Pro Leu  
 370 375 380

<210> 3

<211> 1759

<212> DNA

<213> Mus musculus

<400> 3

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tgcaagata gagatctggc cgccccgggg aatgacgagg gcgctcacac agcccaggga 180
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agctgaacgc aggagccgcc gttacctcta gcagcgccgg ggcagcaccg gtggcccctt 300
gtcagcggga gccccgggac ctggctatgg aaccagtaga atgccctcga ggactgctcc 360
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agctcttcca gagccgtgtg cagcccttcc tggaggaggc agagataacc tttaaactga 480
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actcccggcg ggggccacct ccagaagaac cataactctg tgcctttgtc tactctgtct 1500
aggctgagat gggaccctcc cccgcaccca cctcctggta tgggagggtta tttctaaagt 1560

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tcctatggaa gtggtgggga cccctgcaga gaaagctaga aggtggggct atgacttgga 1620
aagaaaggct ttaccttcca gttagagtaa catccccagt agagccctgc tggctggacc 1680
agttgcatat agaagacatt cccattgct tttaggggacc ttccctggga accaaattca 1740
aataaagaga cttttccaa                                     1759

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<210> 4
<211> 382
<212> PRT
<213> Mus musculus

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<400> 4
Met Glu Pro Val Glu Cys Pro Arg Gly Leu Leu Pro Arg Pro Cys Arg
  1              5              10              15

Val Leu Val Leu Leu Asn Pro Gln Gly Gly Lys Gly Lys Ala Leu Gln
      20              25              30

Leu Phe Gln Ser Arg Val Gln Pro Phe Leu Glu Glu Ala Glu Ile Thr
      35              40              45

Phe Lys Leu Ile Leu Thr Glu Arg Lys Asn His Ala Arg Glu Leu Val
      50              55              60

Cys Ala Glu Glu Leu Gly His Trp Asp Ala Leu Ala Val Met Ser Gly
      65              70              75              80

Asp Gly Leu Met His Glu Val Val Asn Gly Leu Met Glu Arg Pro Asp
      85              90              95

Trp Glu Thr Ala Ile Gln Lys Pro Leu Cys Ser Leu Pro Gly Gly Ser
      100             105             110

Gly Asn Ala Leu Ala Ala Ser Val Asn His Tyr Ala Gly Tyr Glu Gln
      115             120             125

Val Thr Asn Glu Asp Leu Leu Ile Asn Cys Thr Leu Leu Leu Cys Arg
      130             135             140

Arg Arg Leu Ser Pro Met Asn Leu Leu Ser Leu His Thr Ala Ser Gly
      145             150             155             160

Leu Arg Leu Tyr Ser Val Leu Ser Leu Ser Trp Gly Phe Val Ala Asp
      165             170             175

Val Asp Leu Glu Ser Glu Lys Tyr Arg Arg Leu Gly Glu Ile Arg Phe
      180             185             190

Thr Val Gly Thr Phe Phe Arg Leu Ala Ser Leu Arg Ile Tyr Gln Gly
      195             200             205

Gln Leu Ala Tyr Leu Pro Val Gly Thr Val Ala Ser Lys Arg Pro Ala
      210             215             220

Ser Thr Leu Val Gln Lys Gly Pro Val Asp Thr His Leu Val Pro Leu
      225             230             235             240

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<210> 5
<211> 1840
<212> DNA
<213> Homo sapiens
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<400> 5						
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tacgctttta	cagttcactg	tgtaaagaga	gcacgacggc	accgctggaa	gtgggcgcag	180
gtgactttct	ggtgtccaga	ggagcagctg	tgctacttgt	ggctgcagac	cctgcgggag	240
atgctggaga	agctgcagtc	cagaccaaag	catttactgg	tatttatcaa	cccgtttgga	300
ggaaaaggac	aaggcaagcg	gatatatgaa	agaaaagtgg	caccactgtt	caccttagcc	360
tccatcacca	ctgacatcat	cggtaacaaa	ttctatgtta	actatgtaga	agtaattact	420
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atcgtctgtg	tcggcggaga	tggtatgttc	agcgaggtgc	tgacggtctc	gattgggagg	540
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ctccggattg	gaatcattcc	cgcagggtca	acggactcgg	tgtgttactc	caccgtgggc	660
accagcgacg	cagaaacctc	ggcgctgcat	atcgttgttg	gggactcgct	ggccatggat	720
gtgtcctcag	tccaccacaa	cagcacactc	cttcgctact	ccgtgtccct	gctgggctac	780
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atcaatgcc	caaacatgtc	ctgtgcttgt	cgccggagcc	ccaggggcct	ctccccggct	1140
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gaagtttatc	gcgtcaagaa	attccagttt	acgtcgaagc	acatggagga	tggatcacgc	1320
cagcttaagg	agggggggaa	gaagcgcttt	gggcacattt	gcagcagcca	cccctcctgc	1380
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atcgagggtca ggggtccactg ccagctgggtt cgactctttg caccaggaat tgaagagaat 1500
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<210> 6

<211> 471

<212> PRT

<213> Homo sapiens

<400> 6

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Arg His Arg Trp Lys Trp Ala Gln Val Thr Phe Trp Cys Pro Glu Glu
          20              25              30

Gln Leu Cys His Leu Trp Leu Gln Thr Leu Arg Glu Met Leu Glu Lys
          35              40              45

Leu Thr Ser Arg Pro Lys His Leu Leu Val Phe Ile Asn Pro Phe Gly
          50              55              60

Gly Lys Gly Gln Gly Lys Arg Ile Tyr Glu Arg Lys Val Ala Pro Leu
          65              70              75              80

Phe Thr Leu Ala Ser Ile Thr Thr Asp Ile Ile Gly Asn Lys Phe Tyr
          85              90              95

Val Asn Tyr Val Glu Val Ile Thr Glu His Ala Asn Gln Ala Lys Glu
          100             105             110

Thr Leu Tyr Glu Ile Asn Ile Asp Lys Tyr Asp Gly Ile Val Cys Val
          115             120             125

Gly Gly Asp Gly Met Phe Ser Glu Val Leu His Gly Leu Ile Gly Arg
          130             135             140

Thr Gln Arg Ser Ala Gly Val Asp Gln Asn His Pro Arg Ala Val Leu
          145             150             155             160

Val Pro Ser Ser Leu Arg Ile Gly Ile Ile Pro Ala Gly Ser Thr Asp
          165             170             175

Cys Val Cys Tyr Ser Thr Val Gly Thr Ser Asp Ala Glu Thr Ser Ala
          180             185             190

Leu His Ile Val Val Gly Asp Ser Leu Ala Met Asp Val Ser Ser Val
          195             200             205

His His Asn Ser Thr Leu Leu Arg Tyr Ser Val Ser Leu Leu Gly Tyr
          210             215             220

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Gly Phe Tyr Gly Asp Ile Ile Lys Asp Ser Glu Lys Lys Arg Trp Leu  
 225 230 235 240  
 Gly Leu Ala Arg Tyr Asp Phe Ser Gly Leu Lys Thr Phe Leu Ser His  
 245 250 255  
 His Cys Tyr Glu Gly Thr Val Ser Phe Leu Pro Ala Gln His Thr Val  
 260 265 270  
 Gly Ser Pro Arg Asp Arg Lys Pro Cys Arg Ala Gly Cys Phe Val Cys  
 275 280 285  
 Arg Gln Ser Lys Gln Gln Leu Glu Glu Glu Gln Lys Lys Ala Leu Tyr  
 290 295 300  
 Gly Leu Glu Ala Ala Glu Asp Val Glu Glu Trp Gln Val Val Cys Gly  
 305 310 315 320  
 Lys Phe Leu Ala Ile Asn Ala Thr Asn Met Ser Cys Ala Cys Arg Arg  
 325 330 335  
 Ser Pro Arg Gly Leu Ser Pro Ala Ala His Leu Gly Asp Gly Ser Ser  
 340 345 350  
 Asp Leu Ile Leu Ile Arg Lys Cys Ser Arg Phe Asn Phe Leu Arg Phe  
 355 360 365  
 Leu Ile Arg His Thr Asn Gln Gln Asp Gln Phe Asp Phe Thr Phe Val  
 370 375 380  
 Glu Val Tyr Arg Val Lys Lys Phe Gln Phe Thr Ser Lys His Met Glu  
 385 390 395 400  
 Asp Glu Asp Ser Asp Leu Lys Glu Gly Gly Lys Lys Arg Phe Gly His  
 405 410 415  
 Ile Cys Ser Ser His Pro Ser Cys Cys Cys Thr Val Ser Asn Ser Ser  
 420 425 430  
 Trp Asn Cys Asp Gly Glu Val Leu His Ser Pro Ala Ile Glu Val Arg  
 435 440 445  
 Val His Cys Gln Leu Val Arg Leu Phe Ala Arg Gly Ile Glu Glu Asn  
 450 455 460  
 Pro Lys Pro Asp Ser His Ser  
 465 470

<210> 7  
 <211> 522  
 <212> DNA  
 <213> Rattus sp.

<400> 7  
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 cgcaccagct ggcagtggac cctgacctca atggcagggc tgtgcaggac ttccccatca 180

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gtgaactgga atttcttgac tcgataaact tcaacgaaag tgaagccaaa ctgacctcc 360
tggttggtgt gccggatgag gaatctcagg aagttgaacc tggagcattt ccggataagg 420
atgaggtcag aagaccatc tcccagatgg gcaaattggg acaggccccc agggctccgg 480
ggacaagcac aggacatgtt ggtggagttg atagccagga ac 522

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<210> 8  
 <211> 144  
 <212> PRT  
 <213> Rattus sp.

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<400> 8
Phe Leu Ala Ile Asn Ser Thr Asn Met Ser Cys Ala Cys Pro Arg Ser
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Pro Gly Gly Leu Ser Pro Phe Ala His Leu Gly Asp Gly Ser Ser Asp
          20             25             30

Leu Ile Leu Ile Arg Lys Cys Ser Arg Phe Asn Phe Leu Arg Phe Leu
      35             40             45

Ile Arg His Thr Asn Gln Glu Asp Gln Phe Gly Phe Thr Phe Val Glu
      50             55             60

Val Tyr Arg Val Lys Lys Phe Gln Phe Thr Ser Lys His Val Glu Asp
      65             70             75             80

Asp Asp Asn Asp Leu Lys Glu Leu Glu Lys Gln Lys Phe Gly Gln Ile
          85             90             95

Cys Lys Asp Asn Pro Pro Cys Ala Cys Pro Thr Ser Arg Ser Ser Trp
          100             105             110

Asn Cys Asp Gly Glu Val Leu His Ser Pro Ala Ile Glu Val Arg Val
      115             120             125

His Cys Gln Leu Val Arg Leu Phe Ala Arg Gly Ile Glu Glu Glu Ser
      130             135             140

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<210> 9  
 <211> 382  
 <212> DNA  
 <213> Mus musculus

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<400> 9
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aggtcagggt ccactgccag ctggtgcgcc tctttgctcg ggaatcgag gaagagtcac 240
aagcaagaac cccaaagccc aggagctgtc ggccttgagc tcggggagtg tggaaattac 300
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tttgataggt aaatcttggt tt 382

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<210> 10  
 <211> 79  
 <212> PRT  
 <213> Mus musculus

<400> 10  
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                     20                    25                    30  
 Lys Asp Arg Pro Ser Cys Thr Cys Ser Ala Ser Arg Ser Ser Trp Asn  
                     35                    40                    45  
 Cys Asp Gly Glu Val Met His Ser Pro Ala Ile Glu Val Arg Val His  
                     50                    55                    60  
 Cys Gln Leu Val Arg Leu Phe Ala Arg Gly Ile Glu Glu Glu Ser  
     65                    70                    75

<210> 11  
 <211> 326  
 <212> PRT  
 <213> Homo sapiens

<400> 11  
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 Gly Lys Arg Ile Tyr Glu Arg Lys Val Ala Pro Leu Phe Thr Leu Ala  
                     20                    25                    30  
 Ser Ile Thr Thr Asp Ile Ile Gly Asn Lys Phe Tyr Val Asn Tyr Val  
                     35                    40                    45  
 Glu Val Ile Thr Glu His Ala Asn Gln Ala Lys Glu Thr Leu Tyr Glu  
                     50                    55                    60  
 Ile Asn Ile Asp Lys Tyr Asp Gly Ile Val Cys Val Gly Gly Asp Gly  
     65                    70                    75                    80  
 Met Phe Ser Glu Val Leu His Gly Leu Ile Gly Arg Thr Gln Arg Ser  
                     85                    90                    95  
 Ala Gly Val Asp Gln Asn His Pro Arg Ala Val Leu Val Pro Ser Ser  
                     100                    105                    110  
 Leu Arg Ile Gly Ile Ile Pro Ala Gly Ser Thr Asp Cys Val Cys Tyr  
                     115                    120                    125  
 Ser Thr Val Gly Thr Ser Asp Ala Glu Thr Ser Ala Leu His Ile Val  
                     130                    135                    140  
 Val Gly Asp Ser Leu Ala Met Asp Val Ser Ser Val His His Asn Ser  
     145                    150                    155                    160

Thr Leu Leu Arg Tyr Ser Val Ser Leu Leu Gly Tyr Gly Phe Tyr Gly  
 165 170 175  
 Asp Ile Ile Lys Asp Ser Glu Lys Lys Arg Trp Leu Gly Leu Ala Arg  
 180 185 190  
 Tyr Asp Phe Ser Gly Leu Lys Thr Phe Leu Ser His His Cys Tyr Glu  
 195 200 205  
 Gly Thr Val Ser Phe Leu Pro Ala Gln His Thr Val Gly Ser Pro Arg  
 210 215 220  
 Asp Arg Lys Pro Cys Arg Ala Gly Cys Phe Val Cys Arg Gln Ser Lys  
 225 230 235 240  
 Gln Gln Leu Glu Glu Glu Gln Lys Lys Ala Leu Tyr Gly Leu Glu Ala  
 245 250 255  
 Ala Glu Asp Val Glu Glu Trp Gln Val Val Cys Gly Lys Phe Leu Ala  
 260 265 270  
 Ile Asn Ala Thr Asn Met Ser Cys Ala Cys Arg Arg Ser Pro Arg Gly  
 275 280 285  
 Leu Ser Pro Ala Ala His Leu Gly Asp Gly Ser Ser Asp Leu Ile Leu  
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 Thr Asn Gln Gln Asp Gln  
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<210> 12  
 <211> 453  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 12

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 Arg Asn Lys Ser Ile Phe Val Ile Ile Asn Pro Phe Gly Gly Lys Gly  
 35 40 45  
 Lys Ala Lys Lys Leu Phe Met Thr Lys Ala Lys Pro Leu Leu Leu Ala  
 50 55 60  
 Ser Arg Cys Ser Ile Glu Val Val Tyr Thr Lys Tyr Pro Gly His Ala  
 65 70 75 80  
 Ile Glu Ile Ala Arg Glu Met Asp Ile Asp Lys Tyr Asp Thr Ile Ala  
 85 90 95

Cys	Ala	Ser	Gly	Asp	Gly	Ile	Pro	His	Glu	Val	Ile	Asn	Gly	Leu	Tyr	100	105	110
Gln	Arg	Pro	Asp	His	Val	Lys	Ala	Phe	Asn	Asn	Ile	Ala	Ile	Thr	Glu	115	120	125
Ile	Pro	Cys	Gly	Ser	Gly	Asn	Ala	Met	Ser	Val	Ser	Cys	His	Trp	Thr	130	135	140
Asn	Asn	Pro	Ser	Tyr	Ser	Thr	Leu	Cys	Leu	Ile	Lys	Ser	Ile	Glu	Thr	145	150	155
Arg	Ile	Asp	Leu	Met	Cys	Cys	Ser	Gln	Pro	Ser	Tyr	Ala	Arg	Glu	His	165	170	175
Pro	Lys	Leu	Ser	Phe	Leu	Ser	Gln	Thr	Tyr	Gly	Leu	Ile	Ala	Glu	Thr	180	185	190
Asp	Ile	Asn	Thr	Glu	Phe	Ile	Arg	Trp	Met	Gly	Pro	Ala	Arg	Phe	Glu	195	200	205
Leu	Gly	Val	Ala	Phe	Asn	Ile	Ile	Gln	Lys	Lys	Lys	Tyr	Pro	Cys	Glu	210	215	220
Ile	Tyr	Val	Lys	Tyr	Ala	Ala	Lys	Ser	Lys	Asn	Glu	Leu	Lys	Asn	His	225	230	235
Tyr	Leu	Glu	His	Lys	Asn	Lys	Gly	Ser	Leu	Glu	Phe	Gln	His	Ile	Thr	245	250	255
Met	Asn	Lys	Asp	Asn	Glu	Asp	Cys	Asp	Asn	Tyr	Asn	Tyr	Glu	Asn	Glu	260	265	270
Tyr	Glu	Thr	Glu	Asn	Glu	Asp	Glu	Asp	Glu	Asp	Ala	Asp	Ala	Asp	Asp	275	280	285
Glu	Asp	Ser	His	Leu	Ile	Ser	Arg	Asp	Leu	Ala	Asp	Ser	Ser	Ala	Asp	290	295	300
Gln	Ile	Lys	Glu	Glu	Asp	Phe	Lys	Ile	Lys	Tyr	Pro	Leu	Asp	Glu	Gly	305	310	315
Ile	Pro	Ser	Asp	Trp	Glu	Arg	Leu	Asp	Pro	Asn	Ile	Ser	Asn	Asn	Leu	325	330	335
Gly	Ile	Phe	Tyr	Thr	Gly	Lys	Met	Pro	Tyr	Val	Ala	Ala	Asp	Thr	Lys	340	345	350
Phe	Phe	Pro	Ala	Ala	Leu	Pro	Ser	Asp	Gly	Thr	Met	Asp	Met	Val	Ile	355	360	365
Thr	Asp	Ala	Arg	Thr	Ser	Leu	Thr	Arg	Met	Ala	Pro	Ile	Leu	Leu	Gly	370	375	380
Leu	Asp	Lys	Gly	Ser	His	Val	Leu	Gln	Pro	Glu	Val	Leu	His	Ser	Lys	385	390	395

Ile Leu Ala Tyr Lys Ile Ile Pro Lys Leu Gly Asn Gly Leu Phe Ser  
405 410 415

Val Asp Gly Glu Lys Phe Pro Leu Glu Pro Leu Gln Val Glu Ile Met  
420 425 430

Pro Arg Leu Cys Lys Thr Leu Leu Arg Asn Gly Arg Tyr Val Asp Thr  
435 440 445

Asp Phe Asp Ser Met  
450

<210> 13  
<211> 436  
<212> PRT  
<213> *Saccharomyces cerevisiae*

<400> 13  
Leu Leu Ile Asp His Val Ser Arg Lys Ser Arg Ala Asn Thr Gly Glu  
1 5 10 15

Glu Asn Ile Ser Ser Gly Thr Val Glu Glu Ile Leu Glu Lys Ser Tyr  
20 25 30

Glu Asn Ser Lys Arg Asn Arg Ser Ile Leu Val Ile Ile Asn Pro His  
35 40 45

Gly Gly Lys Gly Thr Ala Lys Asn Leu Phe Leu Thr Lys Ala Arg Pro  
50 55 60

Ile Leu Val Glu Ser Gly Cys Lys Ile Glu Ile Ala Tyr Thr Lys Tyr  
65 70 75 80

Ala Arg His Ala Ile Asp Ile Ala Lys Asp Leu Asp Ile Ser Lys Tyr  
85 90 95

Asp Thr Ile Ala Cys Ala Ser Gly Asp Gly Ile Pro Tyr Glu Val Ile  
100 105 110

Asn Gly Leu Tyr Arg Arg Pro Asp Arg Val Asp Ala Phe Asn Lys Leu  
115 120 125

Ala Val Thr Gln Leu Pro Cys Gly Ser Gly Asn Ala Met Ser Ile Ser  
130 135 140

Cys His Trp Thr Asn Asn Pro Ser Tyr Ala Ala Leu Cys Leu Val Lys  
145 150 155 160

Ser Ile Glu Thr Arg Ile Asp Leu Met Cys Cys Ser Gln Pro Ser Tyr  
165 170 175

Met Asn Glu Trp Pro Arg Leu Ser Phe Leu Ser Gln Thr Tyr Gly Val  
180 185 190

Ile Ala Glu Ser Asp Ile Asn Thr Glu Phe Ile Arg Trp Met Gly Pro  
195 200 205

Val Arg Phe Asn Leu Gly Val Ala Phe Asn Ile Ile Gln Gly Lys Lys  
 210 215 220  
 Tyr Pro Cys Glu Val Phe Val Lys Tyr Ala Ala Lys Ser Lys Lys Glu  
 225 230 235 240  
 Leu Lys Val His Phe Leu Glu Asn Lys Asp Lys Asn Lys Gly Cys Leu  
 245 250 255  
 Thr Phe Glu Pro Asn Pro Ser Pro Asn Ser Ser Pro Asp Leu Leu Ser  
 260 265 270  
 Lys Asn Asn Ile Asn Asn Ser Thr Lys Asp Glu Leu Ser Pro Asn Phe  
 275 280 285  
 Leu Asn Glu Asp Asn Phe Lys Leu Lys Tyr Pro Met Thr Glu Pro Val  
 290 295 300  
 Pro Arg Asp Trp Glu Lys Met Asp Ser Glu Leu Thr Asp Asn Leu Thr  
 305 310 315 320  
 Ile Phe Tyr Thr Gly Lys Met Pro Tyr Ile Ala Lys Asp Thr Lys Phe  
 325 330 335  
 Phe Pro Ala Ala Leu Pro Ala Asp Gly Thr Ile Asp Leu Val Ile Thr  
 340 345 350  
 Asp Ala Arg Ile Pro Val Thr Arg Met Thr Pro Ile Leu Leu Ser Leu  
 355 360 365  
 Asp Lys Gly Ser His Val Leu Glu Pro Glu Val Ile His Ser Lys Ile  
 370 375 380  
 Leu Ala Tyr Lys Ile Ile Pro Lys Val Glu Ser Gly Leu Phe Ser Val  
 385 390 395 400  
 Asp Gly Glu Lys Phe Pro Leu Glu Pro Leu Gln Val Glu Ile Met Pro  
 405 410 415  
 Met Leu Cys Lys Thr Leu Leu Arg Asn Gly Arg Tyr Ile Asp Thr Glu  
 420 425 430  
 Phe Glu Ser Met  
 435

<210> 14  
 <211> 380  
 <212> PRT  
 <213> Schizosaccharomyces pombe

<400> 14  
 Cys Trp Val Asp Phe Val Glu Asn Ser Asp Gln Phe Cys Glu Tyr Leu  
 1 5 10 15  
 Leu Asp Val Ala Tyr Lys Gly Ile Lys Arg Ser Arg Arg Phe Ile Val  
 20 25 30

Phe Ile Asn Pro His Gly Gly Lys Gly Lys Ala Lys His Ile Trp Glu  
 35 40 45  
 Ser Glu Ala Glu Pro Val Phe Ser Ser Ala His Ser Ile Cys Glu Val  
 50 55 60  
 Val Leu Thr Arg Arg Lys Asp His Ala Lys Ser Ile Ala Lys Asn Leu  
 65 70 75 80  
 Asp Val Gly Ser Tyr Asp Gly Ile Leu Ser Val Gly Gly Asp Gly Leu  
 85 90 95  
 Phe His Glu Val Ile Asn Gly Leu Gly Glu Arg Asp Asp Tyr Leu Glu  
 100 105 110  
 Ala Phe Lys Leu Pro Val Cys Met Ile Pro Gly Gly Ser Gly Asn Ala  
 115 120 125  
 Phe Ser Tyr Asn Ala Thr Gly Gln Leu Lys Pro Ala Leu Thr Ala Leu  
 130 135 140  
 Glu Ile Leu Lys Gly Arg Pro Thr Ser Phe Asp Leu Met Thr Phe Glu  
 145 150 155 160  
 Gln Lys Gly Lys Lys Ala Tyr Ser Phe Leu Thr Ala Asn Tyr Gly Ile  
 165 170 175  
 Ile Ala Asp Cys Asp Ile Gly Thr Glu Asn Trp Arg Phe Met Gly Glu  
 180 185 190  
 Asn Arg Ala Tyr Leu Gly Phe Phe Leu Arg Leu Phe Gln Lys Pro Asp  
 195 200 205  
 Trp Lys Cys Ser Ile Glu Met Asp Val Val Ser Ser Asp Arg Thr Glu  
 210 215 220  
 Ile Lys His Met Tyr Glu Lys Ser Lys Asn Leu Ala Pro Met Ser Glu  
 225 230 235 240  
 Ser Ser Asp Ser Asp Lys Thr Val Ser Thr Ser Pro Glu Ser His Leu  
 245 250 255  
 Leu Thr Phe Glu Ile Asn Asp Leu Ser Ile Phe Cys Ala Gly Leu Leu  
 260 265 270  
 Pro Tyr Ile Ala Pro Asp Ala Lys Met Phe Pro Ala Ala Ser Asn Asp  
 275 280 285  
 Asp Gly Leu Ile Asp Val Val Ile Val Tyr Ser Lys Gln Phe Arg Lys  
 290 295 300  
 Ser Leu Leu Ser Met Phe Thr Gln Leu Asp Asn Gly Gly Phe Tyr Tyr  
 305 310 315 320  
 Ser Lys His Leu Asn Tyr Tyr Lys Val Arg Ser Phe Arg Phe Thr Pro  
 325 330 335

Val Asn Thr Gly Lys Arg His Tyr Phe Ala Leu Asp Gly Glu Ser Tyr  
                   340                  345                  350

Pro Leu Glu Pro Phe Glu Cys Arg Val Ala Pro Lys Leu Gly Thr Thr  
                   355                  360                  365

Leu Ser Pro Val Ala Gly Phe Gln Leu Leu Asp Ile  
           370                  375                  380

<210> 15

<211> 415

<212> PRT

<213> Caenorhabditis elegans

<400> 15

Cys Arg Ser Asp Ala Glu Glu Asn Glu Gln Leu Thr Ser Val Ile Leu  
   1                  5                  10                  15

Ser Arg Lys Pro Pro Pro Gln Glu Gln Cys Arg Gly Asn Leu Leu Val  
                   20                  25                  30

Phe Ile Asn Pro Asn Ser Gly Thr Gly Lys Ser Leu Glu Thr Phe Ala  
           35                  40                  45

Asn Thr Val Gly Pro Lys Leu Asp Lys Ser Leu Ile Arg Tyr Glu Val  
           50                  55                  60

Val Val Thr Thr Gly Pro Asn His Ala Arg Asn Val Leu Met Thr Lys  
           65                  70                  75                  80

Ala Asp Leu Gly Lys Phe Asn Gly Val Leu Ile Leu Ser Gly Asp Gly  
                   85                  90                  95

Leu Val Phe Glu Ala Leu Asn Gly Ile Leu Cys Arg Glu Asp Ala Phe  
                   100                  105                  110

Arg Ile Phe Pro Thr Leu Pro Ile Gly Ile Val Pro Ser Gly Ser Gly  
           115                  120                  125

Asn Gly Leu Leu Cys Ser Val Leu Ser Lys Tyr Gly Thr Lys Met Asn  
           130                  135                  140

Glu Lys Ser Val Met Glu Arg Ala Leu Glu Ile Ala Thr Ser Pro Thr  
           145                  150                  155                  160

Ala Lys Ala Glu Ser Val Ala Leu Tyr Ser Val Lys Thr Asp Asn Gln  
                   165                  170                  175

Ser Tyr Ala Ser Phe Leu Ser Ile Gly Trp Gly Leu Met Ala Asp Ile  
                   180                  185                  190

Asp Ile Asp Ser Glu Lys Trp Arg Lys Ser Leu Gly His His Arg Phe  
           195                  200                  205

Thr Val Met Gly Phe Ile Arg Ser Cys Asn Leu Arg Ser Tyr Lys Gly  
           210                  215                  220

Arg	Leu	Thr	Tyr	Arg	Pro	Tyr	Lys	Pro	Lys	Gly	Phe	His	Pro	Ser	Ser	225	230	235	240
Asn	Val	Phe	Ser	Val	Tyr	Glu	Lys	Thr	Thr	Gln	Gln	Arg	Ile	Asp	Asp	245	250	255	
Ser	Lys	Val	Lys	Thr	Asn	Gly	Ser	Val	Ser	Asp	Ser	Glu	Glu	Glu	Thr	260	265	270	
Met	Glu	Thr	Lys	Phe	Gln	Asn	Trp	Thr	Leu	Pro	Asp	Ser	Asp	Glu	Thr	275	280	285	
Leu	Ala	Val	Gly	Ser	Ser	Asp	Leu	Glu	Glu	Thr	Val	Val	Ile	Glu	Asp	290	295	300	
Asn	Phe	Val	Asn	Ile	Tyr	Ala	Val	Thr	Leu	Ser	His	Ile	Ala	Ala	Asp	305	310	315	320
Gly	Pro	Phe	Ala	Pro	Ser	Ala	Lys	Leu	Glu	Asp	Asn	Arg	Ile	His	Leu	325	330	335	
Ser	Tyr	Ile	Leu	Trp	Lys	Asp	Ile	Gly	Thr	Arg	Val	Asn	Ile	Ala	Lys	340	345	350	
Tyr	Leu	Leu	Ala	Ile	Glu	His	Glu	Thr	His	Leu	Asp	Leu	Pro	Phe	Val	355	360	365	
Lys	His	Val	Glu	Val	Ser	Ser	Met	Lys	Leu	Glu	Val	Ile	Ser	Glu	Gly	370	375	380	
Ser	His	Val	Val	Leu	Asp	Gly	Glu	Val	Val	Asp	Thr	Lys	Thr	Ile	Glu	385	390	395	400
Val	Ala	Ser	Thr	Lys	Asn	His	Ile	Ser	Val	Phe	Ser	Ser	Thr	Ala		405	410	415	

&lt;210&gt; 16

&lt;211&gt; 4

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Illustrative motif

&lt;400&gt; 16

Asn Glu Gln Lys

1

&lt;210&gt; 17

&lt;211&gt; 4

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence



<220>

<223> Description of Artificial Sequence: Illustrative motif

<400> 17

Asn His Gln Lys

1

<210> 18

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Illustrative motif

<400> 18

Asn Asp Glu Gln

1

<210> 19

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Illustrative motif

<400> 19

Gln His Arg Lys

1

<210> 20

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Illustrative motif

<400> 20

Met Ile Leu Val

1

<210> 21

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Illustrative motif

<400> 21

Met Ile Leu Phe

1

<210> 22

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Illustrative motif

<400> 22

Ser Thr Asn Lys

1

<210> 23

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Illustrative motif

<400> 23

Ser Thr Pro Ala

1

<210> 24

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Illustrative motif

<400> 24

Ser Gly Asn Asp

1

<210> 25

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Illustrative motif

<400> 25

Ser Asn Asp Glu Gln Lys  
1 5

<210> 26

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Illustrative motif

<400> 26

Asn Asp Glu Gln His Lys  
1 5

<210> 27

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Illustrative motif

<400> 27

Asn Glu Gln His Arg Lys  
1 5

<210> 28

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Illustrative motif

<400> 28

Val Leu Ile Met  
1

<210> 29

<211> 182

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: 80432911

&lt;400&gt; 29

Ala Gly Ala Pro Gly Ala Asp Ala Cys Ser Val Pro Val Ser Glu Ile  
 1 5 10 15

Ile Ala Val Glu Glu Thr Asp Val His Gly Lys His Gln Gly Ser Gly  
 20 25 30

Lys Trp Gln Lys Met Glu Lys Pro Tyr Ala Phe Thr Val His Cys Val  
 35 40 45

Lys Arg Ala Arg Arg His Arg Trp Lys Trp Ala Gln Val Thr Phe Trp  
 50 55 60

Cys Pro Glu Glu Gln Leu Cys His Leu Trp Leu Gln Thr Leu Arg Glu  
 65 70 75 80

Met Leu Glu Lys Leu Thr Ser Arg Pro Lys His Leu Leu Val Phe Ile  
 85 90 95

Asn Pro Phe Gly Gly Lys Gly Gln Gly Lys Arg Ile Tyr Glu Arg Lys  
 100 105 110

Val Ala Pro Leu Phe Thr Leu Ala Ser Ile Thr Thr Asp Ile Ile Val  
 115 120 125

Thr Glu His Ala Asn Gln Ala Lys Glu Thr Leu Tyr Glu Ile Asn Ile  
 130 135 140

Asp Lys Tyr Asp Gly Ile Val Cys Val Gly Gly Asp Gly Met Phe Ser  
 145 150 155 160

Glu Val Leu His Gly Leu Ile Gly Arg Thr Gln Arg Ser Ala Gly Val  
 165 170 175

Asp Gln Asn His Pro Arg  
 180